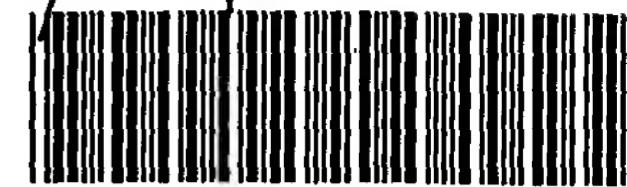


R.Mitra

Re-run

#6
6/25/02

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/935,390A

DATE: 06/25/2002
TIME: 10:24:44

Input Set : N:\paola\US09935390A.RAW
Output Set: N:\CRF3\06252002\I935390A.raw

SEQUENCE LISTING

- 1 (1) GENERAL INFORMATION:
 - 2 (i) APPLICANT: Escobedo, Jaime
 - 3 Quianjin, Hu
 - 4 Garcia, Pablo
 - 5 Williams, Lewis T.
 - 6 Kothakota, Srinivas
 - 7 (ii) TITLE OF INVENTION: Secreted Human Proteins
 - 8 (iii) NUMBER OF SEQUENCES: 38
 - 9 (iv) CORRESPONDENCE ADDRESS:
 - 10 (A) ADDRESSEE: Chiron Corporation
 - 11 (B) STREET: 4560 Horton Street
 - 12 (C) CITY: Emeryville
 - 13 (D) STATE: CA
 - 14 (E) COUNTRY: USA
 - 15 (F) ZIP: 94608-2916
 - 16 (v) COMPUTER READABLE FORM:
 - 17 (A) MEDIUM TYPE: Diskette
 - 18 (B) COMPUTER: IBM Compatible
 - 19 (C) OPERATING SYSTEM: DOS
 - 20 (D) SOFTWARE: FastSEQ for Windows Version 2.0
 - 21 (vi) CURRENT APPLICATION DATA:
 - 22 (A) APPLICATION NUMBER: US/09/935,390A
 - 23 (B) FILING DATE: 22-Aug-2001
 - 24 (C) CLASSIFICATION:
 - 25 (vii) PRIOR APPLICATION DATA:
 - 26 (A) APPLICATION NUMBER: 08/988,671
 - 27 (B) FILING DATE: 1997-12-11
 - 28 (viii) ATTORNEY/AGENT INFORMATION:
 - 29 (A) NAME: Jane E. R. Potter
 - 30 (B) REGISTRATION NUMBER: 33,332
 - 31 (C) REFERENCE/DOCKET NUMBER: 1369.002
 - 32 (ix) TELECOMMUNICATION INFORMATION:
 - 33 (A) TELEPHONE: (510) 923-2718
 - 34 (B) TELEFAX: (510) 655-3542
 - 35 (C) TELEX:
 - 36 (2) INFORMATION FOR SEQ ID NO: 1:
 - 37 (i) SEQUENCE CHARACTERISTICS:
 - 38 (A) LENGTH: 2063 base pairs
 - 39 (B) TYPE: nucleic acid
 - 40 (C) STRANDEDNESS: single
 - 41 (D) TOPOLOGY: linear
 - 42 (ix) FEATURE:

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/935,390A

DATE: 06/25/2002
TIME: 10:24:44

Input Set : N:\paola\US09935390A.RAW
Output Set: N:\CRF3\06252002\I935390A.raw

43 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 44 GAATTGGCA CGAGGCCTCA GTCTTCCAGG GCGGCGGTGG GTGTCCGCTT CTCTCTGCTC 60
 45 TTCGACTGCA CCGCACTCGC GCGTGACCT GACTCCCCCT AGTCAGCTCA GCGGTGCTGC 120
 46 CATGGCGTGG CGGCGGCGCG AAGCCGGCGT CGGGGCTCGC GGCGTGTGG CTCTGGCGTT 180
 47 GCTCGCCCTG GCCCTGTGCG TGCCCGGGGC CGGGGGCCGG GCTCTCGAGT GGTTCTCGGC 240
 48 CGTGGTAAAC ATCGAGTACG TGGACCCGCA GACCAACCTG ACGGTGTGGA GCGTCTCGGA 300
 49 GAGTGGCCGC TTCGGCGACA GCTCGCCCAA GGAGGGCGCG CATGGCCTGG TGGCGTCCC 360
 50 GTGGGCGCCC GGCAGGAGACC TCGAGGGCTG CGCGCCCGAC ACAGCCTTCT TCGTGCCTCGA 420
 51 GCCCGGCGGC CGAGGGGCCG CGCCCTGGGT CGCCCTGGTG GCTCGTGGGG GCTGCACCTT 480
 52 CAAGGACAAG GTGCTGGTGG CGGCGCGGAG GAACGCCTCG GCCGTCTGCC TCTACAATGA 540
 53 GGAGCGCTAC GGGAACATCA CCTTGCCCAT GTCTCACGCG GGAACAGGAA ATATAGTGGT 600
 54 CATTATGATT AGCTATCCAA AAGGAAGAGA AATTTGGAG CTGGTGCAA AAGGAATTCC 660
 55 AGTAACGATG ACCATAGGGG TTGGCACCCG GCATGTACAG GAGTCATCA GCGGTCACTC 720
 56 TGTGGTGTGTT GTGGCCATTG CCTTCATCAC CATGATGATT ATCTCGTTAG CCTGGCTAAT 780
 57 ATTTTACTAT ATACAGCGTT TCCTATATAC TGGCTCTCAG ATTGGAAGTC AGAGCCATAG 840
 58 AAAAGAAACT AAGAAAGTTA TTGGCCAGCT TCTACTTCAT ACTGTAAAGC ATGGAGAAAA 900
 59 GGGAAATTGAT GTGATGCTG AAAATTGTGC AGTGTGTATT GAAAATTCA AAGTAAAGGA 960
 60 TATTATTAGA ATTCTGCCAT GCAAGCATAT TTTTCATAGA ATATGCATTG ACCCATGGCT 1020
 61 TTTGGATCAC CGAACATGTC CAATGTGTA ACTTGATGTC ATCAAAGCCC TAGGATATTG 1080
 62 GGGAGAGCCT GGGGATGTAC AGGAGATGCC TGCTCCAGAA TCTCCTCCTG GAAGGGATCC 1140
 63 AGCTGCAAAT TTGAGTCTAG CTTTACCAAGA TGATGACGGA AGTGTGACCA GCAGTCCACC 1200
 64 ATCAGCCTCC CCTGCTGAAT CTGAGCCACA GTGTGATCCC AGCTTAAAG GAGATGCAGG 1260
 65 AGAAAATACG GCATTGCTAG AAGCCGGCAG GAGTGAATCT CGGCATGGAG GACCCATCTC 1320
 66 CTAGCACACG TGCCCACAGA AGTGGCACCA ACAGAAGTTT GGCTGAACT AAAGGACATT 1380
 67 TTATTTTTT TACTTTAGCA CATAATTGT ATATTTGAAA ATAATGTATA TTATTTTAC 1440
 68 TATTAGATTC TGATTTGATA TACAAAGGAC TAAGATATT TCTCTTGAA GAGACTTTTC 1500
 69 GATTAGTCCT CATATATTAA TCTACTAAAA TAGAGTGTGTT ACCATGAACA GTGTGTTGCT 1560
 70 TCAGACTATT ACAAAAGACAA CTGGGGCAGG TACTCTAATA TAAAGGACAG GTGGTGTTC 1620
 71 TAAATAATTG GCTGCTATGG TTCTGTAAAA ACCAGTTAAT TCTATTTTC AAGGTTTTG 1680
 72 GCAAAGCACA TCAATGTTAG ACTAGTTGAA GTGGAATTGT ATAATTCAAT TCGATAATTG 1740
 73 ATCTCATGGG CTTCCCTGG AGGAAAGGTT TTTTTGTTG TTTTTTTT AAGAACTTGA 1800
 74 AACCTGTAAA CTGAGATGTC TGTAGCTTT TTGCCCATCT GTAGTGTATG TGAAGATTTC 1860
 75 AAAACCTGAG AGCACTTTT CTTGTTTAG AATTATGAGA AAGGCACCTAG ATGACTTTAG 1920
 76 GATTTGCATT TTCCCTTTA TTGCCTCATT TCTGTGACG CCTGTTGGG GAGGGAAATC 1980
 77 TGTTTATTTT TTCTACAAA TAAAAAGCTA AGATTCTATA TCGAAAAAAA AAAAAAAA 2040
 78 AAAAAAAA TTCCCTGCAGGC CGC 2063

80 (2) INFORMATION FOR SEQ ID NO: 2:

81 (i) SEQUENCE CHARACTERISTICS:

82 (A) LENGTH: 1328 base pairs
 83 (B) TYPE: nucleic acid
 84 (C) STRANDEDNESS: single
 85 (D) TOPOLOGY: linear

86 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

87 GAATTGGCA CGAGGTAGGC AAGGGATAAA AAGGCACCTA AGGCCCTTTT GCAATAAGAA 60
 88 GCCAGATGGA TAAAGGAAGT GCTGGTCACC CTGGAGGTGT ACTGGTTGG GGAAGGTCCC 120
 89 CGGCCCCCAC AGCCCTCTGG GGAGCCTCAC CCTGGCTCTC CCCACTCACC TCAGCCCTCA 180
 90 GGCAGCCCT CCACAGGGCC CCTCTCCTGC CTGGACAGCT CTGCTGGTCT CCCCGTCCCC 240
 91 TGGAGAAGAA CAAGGCCATG GGTGGCCCC TGCTGCTGCC CCTGCTGCTC CTGCTGCAGC 300
 92 CGCCAGCATT TCTGCAGCCT GGTGGCTCCA CAGGATCTGG TCCAAGCTAC CTTATGGGG 360

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/935,390A

DATE: 06/25/2002
TIME: 10:24:44

Input Set : N:\paola\US09935390A.RAW
Output Set: N:\CRF3\06252002\I935390A.raw

| | | |
|-----|--|------|
| 93 | TCACTCAACC AAAACACCTC TCAGCCTCCA TGGGTGGCTC TGTGGAAATC CCCTTCTCCT | 420 |
| 94 | TCTATTACCC CTGGGAGTTA GCCATAGTTC CCAACGTGAG AATATCCTGG AGACGGGGCC | 480 |
| 95 | ACTTCCACGG GCAGTCCTTC TACAGCACAA GGCCGCCTTC CATTACAAG GATTATGTGA | 540 |
| 96 | ACCGGCTCTT TCTGAACTGG ACAGAGGGTC AGGAGAGCGG CTTCCCTCAGG ATCTCAAACC | 600 |
| 97 | TGCGGAAGGA GGACCAAGTCT GTGTATTTCT GCCGAGTCGA GCTGGACACC CGGAGATCAG | 660 |
| 98 | GGAGGCAGCA GTTGCAGTCC ATCAAGGGGA CCAAACTCAC CATCACCCAG GCTGTCACAA | 720 |
| 99 | CCACCACCAAC CTGGAGGCC AGCAGCACAA CCACCATAGC CGGCCTCAGG GTCACAGAAA | 780 |
| 100 | GCAAAGGGCA CTCAGAATCA TGGCACCTAA GTCTGGACAC TGCCATCAGG GTTGCATTGG | 840 |
| 101 | CTGTCGCTGT GCTAAAACG GTCATTTGG GACTGCTGTG CCTCCTCCTC CTGTGGTGG | 900 |
| 102 | GGAGAAGGAA AGGTAGCAGG GCGCCAAGCA GTGACTTCTG ACCAACAGAG TGTGGGGAGA | 960 |
| 103 | AGGGATGTGT ATTAGCCCCG GAGGACGTGA TGTGAGACCC GCTTGTGAGT CCTCCACACT | 1020 |
| 104 | CGTTCCCCAT TGGCAAGATA CATGGAGAGC ACCCTGAGGA CCTTTAAAAG GCAAAGCCGC | 1080 |
| 105 | AAGGCAGAAG GAGGCTGGGT CCCTGAATCA CCGACTGGAG GAGAGTTACC TACAAGAGCC | 1140 |
| 106 | TTCATCCAGG AGCATCCACA CTGCAATGAT ATAGGAATGA GGTCTGAACCT CCACTGAATT | 1200 |
| 107 | AAACCACCTGG CATTGGGGG CTGTTTATTA TAGCAGTGCA AAGAGTTCCCT TTATCCTCCC | 1260 |
| 108 | CAAGGATGGA AAAATACAAT TTATTTGCT TACCATAAAA AAAAAAAA AAAAATTCCCT | 1320 |
| 109 | CGGGCCGC | 1328 |

111 (2) INFORMATION FOR SEQ ID NO: 3:

112 (i) SEQUENCE CHARACTERISTICS:

113 (A) LENGTH: 1689 base pairs
114 (B) TYPE: nucleic acid
115 (C) STRANDEDNESS: single
116 (D) TOPOLOGY: linear

117 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

| | | |
|-----|--|------|
| 118 | GAATTGGCA CGAGGGCAAG ATTGATAACA AAACCAATGA ACCTGTGTGG GAGGAAAAC | 60 |
| 119 | TCACTTTCTT CATTACAAT CCCAAGCGCC AGGACCTTGA AGTTGAGGTC AGAGACGAGC | 120 |
| 120 | AGCACCAAGTG TTCCCTGGGG AACCTGAAGG TCCCCCTCAG CCAGCTGCTC ACCAGTGAGG | 180 |
| 121 | ACATGACTGT GAGCCAGCGC TTCCAGCTCA GTAACTCGGG TCCAAACAGC ACCATCAAGA | 240 |
| 122 | TGAAGATTGC CCTGCGGGTG CTCCATCTCG AAAAGCGAGA AAGGCCTCCA GACCACCAAC | 300 |
| 123 | ACTCAGCTCA AGTCAAACGT CCCTCTGTGT CCAAAGAGGG GAGGAAAACA TCCATCAAAT | 360 |
| 124 | CTCATATGTC TGGGTCTCCA GGCCCTGGTG GCAGCAACAC AGTCCATCC ACACCAGTCA | 420 |
| 125 | TTGGGGGCAG TGATAAGCCT GGTATGGAAG AAAAGGCCA GCCCCCTGAG GCCGGCCCTC | 480 |
| 126 | AGGGGCTGCA CGACCTGGGC AGAAGCTCCT CCAGCCTCCT GGCCCTCCCCA GGCCACATCT | 540 |
| 127 | CAGTCAAGGA GCCGACCCCC AGCATCGCCT CGGACATCTC GCTGCCCATC GCCACCCAGG | 600 |
| 128 | AGCTGCGCA AAGGCTGAGG CAGCTGGAAA ACGGGACGAC CCTGGGACAG TCTCCACTGG | 660 |
| 129 | GGCAGATCCA GCTGACCATC CGGCACAGCT CGCAGAGAAA CAAGCTTATC GTGGTCGTGC | 720 |
| 130 | ATGCCTGCAG AAACCTCATT GCCTTCTCTG AAGACGGCTC TGACCCCTAT GTCCGCATGT | 780 |
| 131 | ATTTATTACC AGACAAGAGG CGGTCAAGGAA GGAGGAAAAC ACACGTGTCA AAGAAAACAT | 840 |
| 132 | TAAATCCAGT GTTGTATCAA AGCTTTGATT TCAGTGTTC GTTACCAAGAA GTGCAGAGGA | 900 |
| 133 | GAACGCTCGA CGTTGCCGTG AAGAACAGTG GCGGCTTCCCT GTCCAAAGAC AAAGGGCTCC | 960 |
| 134 | TTGGCAAAGT ATTGGTTGCT CTGGCATCTG AAGAACTTGC CAAAGGCTGG ACCCAGTGGT | 1020 |
| 135 | ATGACCTCAC GGAAGATGGG ACGAGGCCTC AGGCATGAC ATAGCCGCAG CAGGCAGGAG | 1080 |
| 136 | CGCTCCTCTT CAGCGTAGCT CTCCACCTCT ACCCGGAACA CACCCCTCTCA CAGACGTACC | 1140 |
| 137 | AATGTTATTT TTATAATTTC ATGGATTAG TTATACATAC CTTAATAGTT TTATAAAATT | 1200 |
| 138 | GTTGACATTT CAGGCAAATT TGGCCAATAT TATCATTGAA TTTCTGTGT TGGATTCCT | 1260 |
| 139 | CTAGGATTTG GCCAGTTCCCT ACAACGTGCA GTAGGGCGGC GGTAGCTCTT GTGTCTGTGG | 1320 |
| 140 | ACTCTGCTCA GCTGTGTCCG TAGGAGTCGG ATGTGTCTGT GCTTTATTAT GGCTTGT | 1380 |
| 141 | ATATATCACT GAGGTATACT ATGCCATGTA AATAGACTAT TTTTATAAT CTTAACATGC | 1440 |
| 142 | TGGTTAAAT TCAGAAGGAA ATAGATCAAG GAAATATATA TATTTCTTC TAAAACCTTAT | 1500 |

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/935,390A

DATE: 06/25/2002
TIME: 10:24:44

Input Set : N:\paola\US09935390A.RAW
Output Set: N:\CRF3\06252002\I935390A.raw

| | | | | | | | |
|-----|--|------------|-------------|-------------|-------------|------------|------|
| 143 | TAAATTCTGT | TGACAAATAA | TCATTTCAT | CTTGGCAGCA | AAAAGTTCTC | AGTGACCTAT | 1560 |
| 144 | TTTGTGGTGT | TTCTTTTGA | AAAGAAAAGC | TGAAATATTA | TTAAATGCTA | GTATGTTCT | 1620 |
| 145 | GCCCATTATG | AAAGATGAAA | TAAAGTATTTC | AAAATATTAA | AAAAAAAAAA | AAAAAATTCC | 1680 |
| 146 | TGCGGCCGC | | | | | | 1689 |
| 148 | (2) INFORMATION FOR SEQ ID NO: 4: | | | | | | |
| 149 | (i) SEQUENCE CHARACTERISTICS: | | | | | | |
| 150 | (A) LENGTH: 1505 base pairs | | | | | | |
| 151 | (B) TYPE: nucleic acid | | | | | | |
| 152 | (C) STRANDEDNESS: single | | | | | | |
| 153 | (D) TOPOLOGY: linear | | | | | | |
| 154 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: | | | | | | |
| 155 | GAATTGGCA | CGAGGAGCAG | ATCTGCAAGA | GTTCGTTTA | TGGAGGCTGC | TTGGGCAACA | 60 |
| 156 | AGAACAACTA | CCTTCGGGAA | GAAGAGTGCA | TTCTAGCCTG | TCGGGGTGTG | CAAGGTGGC | 120 |
| 157 | CTTGAGAGG | CAGCTCTGGG | GCTCAGGCGA | CTTCCCCCA | GGGCCCCCTCC | ATGGAAAGGC | 180 |
| 158 | GCCATCCAGT | GTGCTCTGGC | ACCTGTCAGC | CCACCCAGTT | CCGCTGCAGC | AATGGCTGCT | 240 |
| 159 | GCATCGACAG | TTTCCTGGAG | TGTGACGACA | CCCCCAACTG | CCCCGACGCC | TCCGACGAGG | 300 |
| 160 | CTGCCTGTGA | AAAATACACG | AGTGGCTTTG | ACGAGCTCCA | GCGCATCCAT | TTCCCCAGCG | 360 |
| 161 | ACAAAGGGCA | CTGCGTGGAC | CTGCCAGACA | CAGGACTCTG | CAAGGAGAGC | ATCCCGCGCT | 420 |
| 162 | GGTACTACAA | CCCCTTCAGC | GAACACTGCG | CCCGCTTAC | CTATGGTGGT | TGTTACGGCA | 480 |
| 163 | ACAAGAACAA | CTTGAGGAA | GAGCAGCAGT | GCCTCGAGTC | TTGTCGCGGC | ATCTCCAAGA | 540 |
| 164 | AGGATGTGTT | TGGCCTGAGG | CGGGAAATCC | CCATTCCCAG | CACAGGCTCT | GTGGAGATGG | 600 |
| 165 | CTGTCGCAGT | GTTCCTGGTC | ATCTGCATTG | TGGTGGTGGT | AGCCATCTTG | GGTTACTGCT | 660 |
| 166 | TCTTCAAGAA | CCAGAGAAAG | GACTTCCACG | GACACCACCA | CCACCCACCA | CCCACCCCTG | 720 |
| 167 | CCAGCTCCAC | TGTCTCCACT | ACCGAGGACA | CGGAGCACCT | GGTCTATAAC | CACACCACGC | 780 |
| 168 | GGCCCCCTTG | AGCCTGGGTC | TCACCGGCTC | TCACCTGGCC | CTGCTTCTG | CTTGCCAAGG | 840 |
| 169 | CAGAGGCCTG | GGCTGGAAA | AACTTTGAA | CCAGACTCTT | GCCTGTTCC | CAGGCCCACT | 900 |
| 170 | GTGCCTCAGA | GACCAGGGCT | CCAGCCCCCTC | TTGGAGAAAGT | CTCAGCTAAG | CTCACGTCT | 960 |
| 171 | GAGAAAGCTC | AAAGGTTTGG | AAGGAGCAGA | AAACCCCTGG | GCCAGAAGTA | CCAGACTAGA | 1020 |
| 172 | TGGACCTGCC | TGCATAGGAG | TTTGGAGGAA | GTGGAGTTT | TGTTTCTCT | GTTCAAAGCT | 1080 |
| 173 | GCCTGTCCCT | ACCCCATGGT | GCTAGGAAGA | GGAGTGGGGT | GGTGTAGAC | CCTGGAGGCC | 1140 |
| 174 | CCAACCTGT | CCTCCCGAGC | TCCTCTTCCA | TGCTGTGC | CCAGGGCTGG | GAGGAAGGAC | 1200 |
| 175 | TTCCCTGTGT | AGTTTGTGCT | GTAAAGAGTT | GCTTTTGTT | TATTTAATGC | TGTGGCATGG | 1260 |
| 176 | GTGAAGAGGA | GGGAAAGAGG | CCTGTTGGC | CTCTCTATCC | TCTCTTCTC | TTCCCCCAAG | 1320 |
| 177 | ATTGAGCTCT | CTGCCCTGTA | TCAGCCCCAC | CCTGGCCTAG | ACCAGCAGAC | AGAGCCAGGA | 1380 |
| 178 | GAAGCTCAGC | TGCATTCCGC | AGCCCCCACC | CCCAAGGTT | TCCAACATCA | CAGCCCAGCC | 1440 |
| 179 | CGCCCCACTGG | GTAATAAAAG | TGGTTTGTGG | AAAAAAAAAA | AAAAAAAAAA | AAGTCCTGCG | 1500 |
| 180 | GCCGC | | | | | | 1505 |
| 182 | (2) INFORMATION FOR SEQ ID NO: 5: | | | | | | |
| 183 | (i) SEQUENCE CHARACTERISTICS: | | | | | | |
| 184 | (A) LENGTH: 2002 base pairs | | | | | | |
| 185 | (B) TYPE: nucleic acid | | | | | | |
| 186 | (C) STRANDEDNESS: single | | | | | | |
| 187 | (D) TOPOLOGY: linear | | | | | | |
| 188 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: | | | | | | |
| 189 | GAATTGGCA | CGAGGGCCAT | GGCCGGGCTA | TCCCGCGGGT | CCGCGCGCGC | ACTGCTGCC | 60 |
| 190 | GCCCTGCTGG | CGTCGACGCT | GTGGCGCTG | CTCGTGTGC | CCGCGCGGGG | TCGCGCGGC | 120 |
| 191 | CGGGACCACG | GGGACTGGGA | CGAGGCCTCC | CGGCTGCCGC | CGCTACCACC | CCGCGAGGAC | 180 |
| 192 | CGGGCGCGCG | TGGCCCGCTT | CGTGACGCAC | GTCTCCGACT | GGGGCGCTCT | GGCCACCATC | 240 |
| 193 | TCCACGCTGG | AGGCGGTGCG | CGGCCGGCCC | TTCGCCGACG | TCCTCTCGCT | CAGCGACGGG | 300 |

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/935,390A

DATE: 06/25/2002
TIME: 10:24:44

Input Set : N:\paola\US09935390A.RAW
Output Set: N:\CRF3\06252002\I935390A.raw

| | | |
|-----|--|------|
| 194 | CCCCCGGGCG CGGGCAGCGG CGTGCCTAT TTCTACCTGA GCCCGCTGCA GCTCTCCGTG | 360 |
| 195 | AGCAACCTGC AGGAGAATCC ATATGCTACA CTGACCATGA CTTTGGCACA GACCAACTTC | 420 |
| 196 | TGCAAGAAC ATGGATTGA TCCACAAAGT CCCCTTGTC TTCACATAAT GCTGTCAGGA | 480 |
| 197 | ACTGTGACCA AGGTGAATGA AACAGAAATG GATATTGCAA AGCATTGTT ATTCAATTGCA | 540 |
| 198 | CACCCCTGAGA TGAAAACCTG GCCTTCCAGC CATAATTGGT TCTTGCTAA GTGAAATATA | 600 |
| 199 | ACCAATATCT GGGTCCTGGA CTACTTTGGT GGACCAAAAA TCGTGACACC AGAAGAATAT | 660 |
| 200 | TATAATGTCA CAGTTCAGTG AAGCAGACTG TGGTGAATT AGCAACACTT ATGAAGTTTC | 720 |
| 201 | TTAAAGTGGC TCATACACAC TTAAAAGGCT TAATGTTCT CTGGAAAGCG TCCCAGAATA | 780 |
| 202 | TTAGCCAGTT TTCTGTCACA TGCTGGTTG TTTGCTGCT TGTTTACTTG CTTGTTTAC | 840 |
| 203 | AATAGAGTTG ACCTGTTATT GGATTTCCTG GAAGATGTGG TAGCTACTTT TTTCCTATTT | 900 |
| 204 | TGAAGCCATT TTCGTAGAGA AATATCCCTC ACTATAATCA AATAAGTTT GTCCCACCAA | 960 |
| 205 | TTCCAAAGAT GTTCCAGTG GTGCTCTGA AGAGGAATGA GTACCAAGTT TAAATTGCC | 1020 |
| 206 | ATTGGCATT GAAGGTAGTT GAGTATGTGT TCTTATTCC TAGAAGCCAC TGTGCTTGGT | 1080 |
| 207 | AGAGTGCATC ACTCACCAACA GCTGCCTCTT GAGCTGCCGT AGCCTGGTGC AAAAGGATTG | 1140 |
| 208 | GCCCCCATTA TGGTGCCTCT GAATAAACTC TGCCAAGATA GACAAACAAT GATGAAACTC | 1200 |
| 209 | AGATGGAGCT TCCTACTCAT GTTGATTAT GTCTCACAAT CCTGGTATT GTTAATTCAA | 1260 |
| 210 | CATAGGGTGA AACTATTCT GATAAAAGAAC TTTGAAAAA CTTTTATAC TCTAAAGTGA | 1320 |
| 211 | TACTCAGAAC AAAAGAAAGT CATAAAACTC CTGAATTAA TTTCCCCACC TAAGTCGAGA | 1380 |
| 212 | CAGTATTATC AAAACACATG TGCACACAGA TTATTTTG GCTCCAAAAC TGGATTGCAA | 1440 |
| 213 | AAGAAAGAGG AGAGATATT TGTGTGTCC TGGTATTCTT TTATAAGTAA AGTTACCCAG | 1500 |
| 214 | GCATGGACCA GCTTCAGCCA GGGACAAAAT CCCCTCCCAA ACCACTCTCC ACAGCTTTT | 1560 |
| 215 | AAAAATACTT CTACTCTAA CAATTACCTA AGGTTCCCTC AAACCCCCC AACTCTTAAT | 1620 |
| 216 | AGCTTCTAGT GCTGCTACAA TCTAAGTCAG GTCACCAGAG GGAAGAGAAC ATGGCATTAA | 1680 |
| 217 | AAGAATCACA TCTTCAGAAC AGAAGACACT AATATTATTA CCCATATACA TGATTTCAGA | 1740 |
| 218 | AGATGACATA AGATTCCCTCT TAAAGAGGAA ATGTCAGGAA TCAAGCCACT GAATCCTTAA | 1800 |
| 219 | AGAGAAAAGT TGAATATGAG TCATTGTGTC TGAAAAGTGC AAAGTGAAC TAACTGAGAT | 1860 |
| 220 | CCAGCAAACA GGTTCTGTT AAGAAAAATA ATTTATACTA AATTTAGTAA AATGGACTTC | 1920 |
| 221 | TTATTCAAAG CATCAATAAT TAAAAGAATT ATTTAAAAA AAAAAAAA AAAAAAAA | 1980 |
| 222 | AAAAAAAAT TCCTGCGGCC GC | 2002 |

224 (2) INFORMATION FOR SEQ ID NO: 6:

225 (i) SEQUENCE CHARACTERISTICS:

226 (A) LENGTH: 1322 base pairs
227 (B) TYPE: nucleic acid
228 (C) STRANDEDNESS: single
229 (D) TOPOLOGY: linear

230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

| | | |
|-----|---|-----|
| 231 | GAATTGGCA CGAGGGCCAC GACTCTGCTG GCATTTCTTC TATAGCCACT GGAATCTGAT | 60 |
| 232 | CCTGATTGTC TTCCACTACT ACCAGGCCAT CACCACTCCG CCTGGGTACC CACCCAGGG | 120 |
| 233 | CAGGAATGAT ATCGCCACCG TCTCCATCTG TAAGAAGTGC ATTACCCCA AGCCAGCCCG | 180 |
| 234 | AACACACCAC TGCAGCATCT GCAACAGGTG TGTGCTGAAG ATGGATCACC ACTGCCCTG | 240 |
| 235 | GCTAAACAAT TGTGTGGGCC ACTATAACCA TCGGTACTTC TTCTCTTCT GCTTTTCAT | 300 |
| 236 | GACTCTGGGC TGTGTCTACT GCAGCTATGG AAGTTGGGAC CTTTCCGGG AGGCTTATGC | 360 |
| 237 | TGCCATTGAG AAAATGAAAC AGCTCGACAA GAACAAACTA CAGGCGGTTG CCAACCAGAC | 420 |
| 238 | TTATCACCAG ACCCCACCAC CCACCTTCTC CTTTCGAGAA AGGATGACTC ACAAGAGTCT | 480 |
| 239 | TGTCTACCTC TGGTTCTGT GCAGTTCTGT GGCACCTGCC CTGGGTGCC TAACGTATG | 540 |
| 240 | GCATGCTGTT CTCATCAGTC GAGGTGAGAC TAGCATCGAA AGGCACATCA ACAAGAAGGA | 600 |
| 241 | GAGACGTCGG CTACAGGCCA AGGGCAGAGT ATTTAGGAAT CCTTACAAC ACGGCTGCTT | 660 |
| 242 | GGACAACTGG AAGGTATTCC TGGGTGTGGA TACAGGAAGG CACTGGCTTA CTCGGGTGCT | 720 |
| 243 | CTTACCTTCT ACTCACTTGC CCCATGGGAA TGGAATGAGC TGGGAGCCCC CTCCTGGGT | 780 |

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/935,390A

DATE: 06/25/2002

TIME: 10:24:45

Input Set : N:\paola\US09935390A.RAW

Output Set: N:\CRF3\06252002\I935390A.raw

L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:43 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1
L:678 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20
L:737 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21
L:784 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22
L:831 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23
L:866 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
L:903 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:938 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:1005 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:1046 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28
L:1083 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:1126 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:1167 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31
L:1224 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32
L:1265 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33
L:1322 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34
L:1373 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35
L:1418 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=36
L:1455 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=37
L:1524 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=38